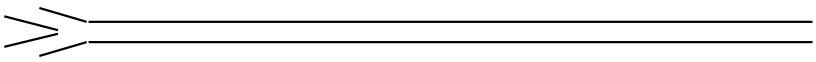
Appendix D



Suggested Data Elements

DEEMS VERSION 1.0
DATA ELEMENT DICTIONARY

DATA ELEMENT	DESCRIPTION
Acid_Reaction	
Format: Limited_List	
Record: **Sample_and_Method**	Reaction of the sample to acid. Examples: Weak, Strong.
Record: **Handling**	Same as in a Sample_and_Method record.
Aliquot_Amount	
Format: Numeric	
Record: **Analysis**	The amount of sample used for this analysis. This usage of the word aliquot is not consistent with its dictionary definition, but is standard for many chemists.
Aliquot_Amount_Units	
Format: Limited_List	
Record: **Analysis**	Units for Aliquot_Amount.
Alternate_Lab_Analysis_ID	
Format: Identifier	
Record: **Analysis**	Alternate lab identifier for an analysis. This value is for information purposes only to facilitate tracking back into the lab's systems.
Alternate_Lab_Sample_ID	
Format: Identifier	
Record: **Sample_and_Method**	Alternate lab identifier for a sample. This value is for information purposes only to facilitate tracking back into the lab's systems. It might be used when the lab has both a lab-wide sample id and a different, department specific for particular methods.
Amount_Added	
Format: Numeric	
Record: **Result**	Specifies a known amount of analyte that has been spiked into the aliquot. Used with method QC samples of QC_Category Blank_Spike, Spike, Spike_Duplicate and Blank_Spike_Duplicate.

DATA ELEMENT	DESCRIPTION
	Spike analytes should have 'Analyte_Type=Spike'.
Record: **Analyte**	Same as in a Result record extended so Amount_Added can now refer to spikes, surrogates, tracers, standard additions, and calibration standards where known amounts of analytes have been added to samples for QC purposes. 'Analyte_Type=Spike' should be specified for spiked analytes unless some other Analyte_Type is more appropriate or which analytes were spiked is known based on a QC_Type associated with this data.
Amount_Added_Error Format: Numeric Record: **Result**	The one sigma error in the estimate of the Amount_Added.
Record: **Analyte**	Same as in a Result record.
Amount_Added_Error_Units Format: Limited_List Record: **Result**	Units for Amount_Added_Error. If the client specifies that the Amount_Added_Error_Units must be the same as the Amount_Added_Units, the Amount_Added_Error_Units need not be specified.
Record: **Analyte**	Same as in a Result record.
Amount_Added_Units Format: Limited_List Record: Result	Units for Amount_Added. If the client specifies that the Amount_Added_Units must be the same as the Result_Units, the Amount_Added_Units need not be specified.
Record: **Analyte**	Same as in a Result record.

DATA ELEMENT	DESCRIPTION
Analysis_Batch Format: Identifier Record: **Analysis**	An identifier for a batch of analyses on one instrument associated with the level of detail at which the instrument is checked to be in control. Example: Analyses QC'd by the same continuing calibration or similar_QC.
Analysis_Duration Format: Numeric Record: **Analysis**	The duration of the instrumental analysis. Example: Radiochemical count time.
Record: **Analyte**	The duration of the instrumental analysis for this analyte. Example: ICP integration time.
Analysis_Duration_Units Format: Limited_List Record: **Analysis**	Units for Analysis_Duration.
Record: **Analyte**	Units for Analysis_Duration.
Analysis_Group Format: Identifier Record: **Analysis_Group**	*Required* A lab defined code for an Analysis_Group. If an Analysis_Group is needed to fully identify what was done, the Lab_Analysis_ID's in related Analysis records might be constructed as the Analysis_Group code combined with a suffix. For example, in dual column GC, the GC data system often has a code for the pair of analyses, which can be used as the Analysis_Group identifier. Adding a column number to this identifier gives a suitable Lab_Analysis_ID.
Record: **Analysis**	The Analysis_Group this analysis is part of. The Client_Method_ID or Analysis_Type should imply whether or not an Analysis_Group is needed.

DATA ELEMENT	DESCRIPTION
Record: **Result**	If there is any ambiguity about which analyses underlie this result, the Analysis_Group that identifies these analyses.
Analysis_Request_ID Format: Identifier Record: **Sample_and_Method**	Client's code for the paperwork that authorizes the analyses of specific samples by listed methods. Sometimes this is identical to the chain of custody identifier.
Analysis_Type Format: Limited_List Record: Analysis	*Conditionally Required* Client's code to define the type of analysis. This code is only needed if more than one analysis is done per Analysis_Group. Examples: 1. For dual column GC, this code identifies the type of column (first or second) used. In current CLP practice, the column identifier (really a manufacturer's code) might be used for this value in lieu of a CLP-specified value. 2. If several measurements are averaged to produce the final result, codes for the first, second, ... analyses done. 3. When doing a method of standard additions, this code identifies the first, second,...analyses done. For example, CLP codes are MSA0, MSA1,... 4. When every sample is spiked to measure the linear response of the method, this code identifies the spiked and unspiked analyses. This technique is used in some radiochemistry methods (some versions of Tritium and (Total Uranium), but it is rare to report the spiked analysis except in the raw data, so no standard codes exist.

DATA ELEMENT	DESCRIPTION
	5. When the method involves a secondary measurement of some factor necessary to compute the result, this code identifies the secondary analysis. For example, some methods for PU-241 by liquid scintillation require a separate alpha count of the tracer to determine the yield. 6. If client rules are to report only one (best) result after reanalyses or dilutions, this code could classify each analysis in these terms.
Record: **Analysis_Group**	Client's code to define the type of Analysis_Group. This code is only needed if more than one type of Analysis_Group applies to one Sample_and_Method or Instrument_QC record. Example: For CLP Inorganics Method of Standard Additions, Analysis_Groups are needed for normal and Analytical Spike groups as well as the MSA groups.
Analyst Format: Text Record: **Handling**	Name or initials for the analyst doing the work described in this record.
Record: **Analysis**	Same as in a Handling record.
Record: **Cleanup**	Same as in a Handling record.
Analyte_Name Format: Text Record: **Result**	Lab assigned chemical name for the analyte. For GCMS TICs (Tentatively Identified Compounds), this name may come from a mass spectral library.
Record: **Analyte**	Same as in a Result record
Record: **Analyte_Comparison**	Analyte_Name for the analyte to compare to.
Record: **Peak_Comparison**	Analyte_Name for the analyte to compare to.
Analyte_Type Format: Limited_List	Conditionally Required

DATA ELEMENT	DESCRIPTION
Record: **Result**	In a Result record, required values, ignoring case, are: Spike -- This analyte has been spiked. TIC -- This analyte is non-routine and is tentatively identified. This field is not used for a routine analyte.
Record: **Analyte**	Same as in a Result record with the following required values, ignoring case, in addition to Spike and TIC: Internal_Standard -- Defined as per CLP usage. Surrogate -- Defined as per CLP usage. System_Monitoring_Compound_ -- Defined as per CLP usage. Tracer -- Like an internal standard except it is added at the beginning of sample preparation, rather than just before analysis.
Analytical_Error Format: Numeric Record: **Result**	The estimated one sigma error in the result due to all effects related to analysis by the lab.
Record: **Analyte**	Same as in a Result record extended to anything considered to be the result of any analysis. Within an Analysis_Group record, applies to a mean or other value computed from several analyses.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Analytical_Error_Units Format: Limited_List Record: Result	Units for Analytical_Error. If the client specifies that the Analytical_Error_Units must be the same as the Result_Units, the Analytical_Error_Units need not be specified.

DATA ELEMENT	DESCRIPTION
Record: Analyte	Same as in a Result record.
Record: Peak	Same as in a Result record.
Analyzed Format: Date Record: **Analysis**	Analysis date.
Apparatus_ID Format: Identifier Record: **Analysis**	The lab's code for the apparatus used to process an aliquot. Example: An identifier for a Purge and Trap device.
Record: **Handling**	The lab's code for the apparatus used to process a sample. Example: An identifier for a TCLP device.
Record: **Cleanup**	The lab's code for the apparatus used to cleanup an aliquot. Example: An identifier for a GPC device.
Artifacts Format: Text Record: **Sample_and_Method**	Method defined concept used to report anomalies in the sample.
Record: **Handling**	Same as in a Sample_and_Method record.
Autosampler Format: Limited_List Record: Analysis	Whether an autosampler was used.
Background_Correction Format: Limited_List Record: **Analysis**	Whether or not background correction was done.
Background_Raw_Data Format: Limited_List	

DATA ELEMENT	DESCRIPTION
Record: **Analysis**	Whether raw data was generated when background correction was done. Example, used for CLP Inorganics ICP.
Background_Type Format: Limited_List Record: **Analysis**	The type of background correction done. Example: CLP Inorganics Furnace AA distinguishes Smith-Hieftje, Deuterium Arc, and Zeeman types.
Record: **Analyte**	Same as in an Analyte record, except specific to an analyte.
Record: **Peak**	Same as in an Analyte record, except specific to a peak.
Bias_Error_Ratio Format: Numeric Record: **Result**	For method QC of QC_Category, Blank_Spike, and Blank_Spike_Duplicate, the difference between the result and amount added as a fraction of the square root of sum of squares of the one sigma analytical error and one sigma amount added error.
Record: **Analyte**	Same as in Result records except applied to the results of analyses in an analysis group rather than a QC sample and original pair.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Billing_ID Format: Identifier Record: **Sample_and_Method**	Client's code to submit with the data for billing purposes.
Boiling_Point Format: Numeric Record: **Sample_and_Method**	Boiling point of the sample.

DATA ELEMENT	DESCRIPTION
Record: **Handling**	Same as in a Sample_and_Method record.
Boiling_Point_Units	
Format: Limited_List	
Record: **Sample_and_Method**	Units for the Boiling_Point.
Record: **Handling**	Units for the Boiling_Point.
Bottles	
Format: Numeric	
Record: **Sample_and_Method**	Number of sample bottles.
Bottle_ID	
Format: Identifier	
Record: **Sample_and_Method**	Identifier for the bottle containing the sample being analyzed. May repeat in one record if several bottles are treated as one sample.
Record: **Analysis**	Identifier for the bottle containing the aliquot being analyzed. May repeat in one record if several bottles are used to prepare one aliquot.
Calibration_Factor	
Format: Numeric	
Record: **Analyte**	Factor used to convert measured to final results.
Record: **Peak**	Same as in an Analyte record, except applied to a single peak.
Calibration_Factor_Units	
Format: Limited_List	
Record: **Analyte**	Units for Calibration_Factor
Record: **Peak**	Units for Calibration_Factor.
CAS_Number	
Format: Identifier	
Record: **Result**	The Chemical Abstract Service number for the analyte. Only use values assigned by the Chemical Abstracts Service with this field.

DATA ELEMENT	DESCRIPTION
	Values can be entered with or without hyphen delimiters.
Record: **Analyte**	Same as in a Result record.
Record: Analyte_Comparison	CAS_Number for the analyte to compare to.
Record: Peak_Comparison	CAS_Number for the analyte to compare to.
Checksum Format: Numeric Record: **All**	A value based on all other data in a record that can be used to check EDD integrity. This field can be used in any record. Its value applies to the record it is in. The required algorithm to compute the data for this field is as follows: For all data in a record, starting with the record type line, ending before the next record type line or end of the data stream, and ignoring: 1. The carriage return and linefeed at the end of each line. 2. Any optional leading spaces in 'record:' and 'field='lines. 3. The entire line with the checksum field. Compute the sum of the ASCII codes of all non-ignored characters. Report this sum as an integer following the 'checksum='.
Clarity Format: Limited_List Record: **Sample_and_Method**	Clarity of the sample as received. Examples: Clear, Cloudy, Opaque.
Record: **Handling**	Clarity of the sample after the handling described in this record.

DATA ELEMENT	DESCRIPTION
Record: **Analysis**	Clarity of the aliquot after preparation.
Record: **Cleanup**	Clarity of the aliquot after the cleanup described in this record.
Cleaned_Up Format: Date Record: **Cleanup**	Date of cleanup of this aliquot.
Cleanup_Batch Format: Identifier Record: **Cleanup**	The lab's identifier for a batch of aliquots cleaned up together. The definition of a cleanup batch depends on the method but might be linked to cleanup specific QC samples such as GPC calibrations. Example: All analyses associated with one GPC calibration would be in one Cleanup_Batch of Cleanup_Type GPC. The Instrument_QC in the batch might have QC_Type GPC_Calibration.
Cleanup_ID Format: Identifier Record: **Cleanup**	The lab's identifier for this cleanup event for this aliquot.
Cleanup_Type Format: Limited_List Record: **Instrument_QC**	*For Portability* For instrument QC with QC_Linkage 'Cleanup_Batch', a code that identifies the type of cleanup this QC pertains to. The field's value must match that specified as the Cleanup_Type for cleanups of associated analyses.
Record: **Cleanup**	A code the specifies the type of cleanup. Valid values might be specified for each Client_Method_ID. Examples: GPC, Florisil, and Sulfur.
Client_Analysis_ID Format: Identifier Record: **Analysis**	An optional client defined identifier for this analysis.

DATA ELEMENT	DESCRIPTION
	Examples: In the CLP, required analysis identifiers like VBLKxy and INDALxy.
Client_Analyte_ID Format: Identifier Record: **Result**	*Required* The client's code for the analyte. This code should be the basis on which the client recognizes the analyte.
Record: **Analyte**	Same as in a Result record.
Record: **Analyte_Comparison**	Client_Analyte_ID for the analyte to compare to.
Record: **Peak_Comparison**	Client_Analyte_ID for the analyte to compare to. If not specified, it is assumed to be the same as the analyte for the Peak record this Peak_Comparison record is in.
Client_ID Format: Limited_List Record: **Sample_and_Method**	*For Portability* An identifier for the person or organization ordering the analysis. Often client defined. This value is necessary to allow one client to read data reported in a format specified by another. To be fully reliable, Client_ID's must be unique across all potential clients. Someday they might be assigned by a central group. Examples: EPA Region, AFCID (Air Force Client ID), Customer.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Client_Method_ID Format: Limited_List Record: **Sample_and_Method**	*Required* The client's code for the work to be done. The complete code many be a composite of a number of values, such as a CLP method code (OLM02.0), a fraction (Semivolatiles) and a level (Low). Full details about the meaning of fields and relationships in the EDD are defined relative to the

DATA ELEMENT	DESCRIPTION
	combination of this value and the Matrix_ID. Values for the Client_Method_ID and Matrix_ID should be specified in the client's DEEMS implementation, possibly by referencing the Client's Statement of Work (SOW). The Client_Method_ID is not a generic method number that only identifies the analytical process. It must address issues such as the number and types of QC samples expected, what types of reanalyses and dilutions are expected, and how to report final results when reanalyses and\or dilutions are done. NOTE: The 'Client_ID' is required to make this code unique across client boundaries.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Client_Name	
Format: Text	
Record: **Sample_and_Method**	Descriptive name for the person or organization ordering the analysis. May be lab defined. Examples: EPA Region, AFCID (Air Force Client ID), Customer.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Client_Reanalysis_Type	
Format: Limited_List	*Conditionally Required*
Record: **Sample_and_Method**	If the client wants results for reanalyses done by this method to be reported separately, the client defined code to identify the reanalysis. The Client_Method_ID, Client_Sample_ID and Client_Reanalysis_Type together should uniquely identify the data associated with this record except possibly for lab generated QC samples. Reanalysis is defined as generally as possible to include notions such as reextraction, dilution, and rework. Example: DL, RE and REDL as used in the CLP.

DATA ELEMENT	DESCRIPTION
Client_Sample_ID Format: Identifier Record: Sample_and_Method	*Required* Client's identifier for a sample. This should be the basis on which the client identifies the sample. However, not all clients define values for lab generated QC samples. Example: EPA Sample Number
Collected Format: Date Record: **Sample_and_Method**	Date the sample was collected. If collected over a range of dates, this is the start date.
Collected_End Format: Date Record: **Sample_and_Method**	If the sample was collected over a range of dates, the end of the collection period.
Color Format: Limited_List Record: **Sample_and_Method** Record: **Handling** Record: **Analysis** Record: **Cleanup**	Color of the sample as received. Color of the sample after the handling described by this record. Color of the sample after preparation Color of the aliquot after the cleanup described by this record.
Column Format: Text Record: **Analysis** Record: **Cleanup**	Name of the column used for analysis Name of the column used for this Cleanup. Example: GPC column identifier.
Column_Internal_Diameter Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analysis**	Internal diameter of the analytical column.
Column_Internal_Diameter_Units Format: Limited_List Record: **Analysis**	Units for Column_Internal_Diameter.
Comment Format: Text Record: **All**	*Repeals OK* A free-form comment that can occur in any record. Its value applies to the data in the record it is in. The exact location of a Comment field in a record is not significant. There can be many Comment fields in one record. The order in which these occur may be significant to their meaning. Comment fields, as opposed to ';comments', are meant to be related to data reported in other fields in the same record. Readers are not required to take any action based on these comments, but they might choose to record them as text comments in their database.
Composite Format: Limited_List Record: **Sample_and_Method**	If the sample is a composite.
Conductance Format: Numeric Record: **Sample_and_Method**	Conductance of the sample.
Conductance_units Format: Limited_List Record: **Sample_and_Method**	Units for Conductance.
Confirmation_Analysis_ID Format: Identifier Record: **Analysis**	Identifier for an analysis that confirms the results of this analysis. Example: Confirmatory GCMS Lab File ID in CLP Pesticides.

DATA ELEMENT	DESCRIPTION
Record: **Analysis_Group**	Same as in Analysis record except confirming results from this Analysis_Group.
Consolidation Format: Limited_List Record: **Sample_and_Method**	Degree of consolidation of the sample. Weak, Moderate etc.
Correction_Factor Format: Numeric Record: **Analyte_Comparison**	The correction factor for the peak this record is in, based on interanalyte effects from the analyte named in this record.
Correlation_Coefficient Format: Numeric Record: **Analyte**	The correlation coefficient resulting from linear regression of data. Used for an analyte in an Analysis_Group record.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Counting_Error Format: Numeric Record: **Result**	For methods based on counting discrete events, such as are common in radiochemistry, the one sigma error in the net count rate, usually scaled to the same units as the result. A more precise definition of Counting_Error may specified for each method.
Record: **Analyte**	Same as in a Result record extended to anything considered to be the result of any analysis. Within an Analysis_Group record, applies to a mean or other value computed from several analyses.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Counting_Error_Units Format: Limited_List Record: **Result**	Units for Counting_Error.

DATA ELEMENT	DESCRIPTION
	If the client specifies that the Counting_Error_Units must be the same as the Result_Units, the Counting_Error_Units need not be specified.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Created	
Format: Date	
Record: **Sample_and_Method**	The date a QC sample was generated or derived in the lab.
Custody_ID	
Format: Identifier	
Record: **Sample_and_Method**	Client's code for the chain of custody document associated with receipt of this sample in the lab.
Date_Format	
Format: Limited_List	
Record: **Header**	A value that specifies the format of all date/time values that follow this Header record. Allowed values for this field are listed with the description of allowed date formats for field values. A required Date_Format value may be specified by the client or implementation.
Density	
Format: Numeric	
Record: **Sample_and_Method**	The density of the sample.
Record: **Handling**	The density of the sample after the handling described by this record.
Detection_Limit	
Format: Numeric	
Record: **Result**	Detection limit for the analyte being measured.
Record: Analyte	Same as in a Result record extended to anything considered to be the result of any analysis. Within an Analysis_Group record, applies to a mean or other value computed from several analyses. For

DATA ELEMENT	DESCRIPTION
	Instrument_QC, the value might be an instrument detection limit.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Detection_Limit_Type	
Format: Limited_List	
Record: **Result**	One of a list of client defined acronyms that specify the type of detection limit. Examples: CRDL, MDA, MDL, IDL.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Detection_Limit_Units	
Format: **Limited_List**	
Record: **Result**	Units for Detection_Limit.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Detector_Type	
Format: Limited_List	
Record: **Analysis**	The type of detector used in the instrumental analysis. This is not an instrument identifier. Examples: FID, GCMS.
Difference_Error_Ratio	
Format: Numeric	
Record: **Result**	The absolute value of the difference of two values as fraction of the square root of sum of squares of their one sigma analytical errors. Used with method QC of QC_Category Duplicate, Serial_Dilution,Spike_Duplicate and Blank_Spike_Duplicate.

DATA ELEMENT	DESCRIPTION
Record: **Analyte**	Same as in Result records except applied to the results of analyses in an analysis group rather than a QC sample and original pair.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Dilution	
Format: Numeric	
Record: **Analysis**	The overall dilution of the sample aliquot. A value of one should correspond to nominal conditions for the method. Values less than one correspond to concentrations. Exactly which factors are included in the dilution may depend on the method.
Dilutions	
Format: Numeric	
Record: **Analysis**	Number of dilutions done to this aliquot.
Drift	
Format: Numeric	
Record: **Analysis**	The difference between the actual location of a peak and its predicted position. For alpha spectroscopy, Drift is computed using the tracer peak.
Record: **Analyte**	Same as in an Analysis record except applied to a specific analyte.
Record: **Peak**	Same as in an Analysis record except applied to a specific peak.
Drift_Units	
Format: Limited_List	
Record: **Analyte**	Units for Drift.
Record: **Analysis**	Units for Drift.
Record: **Peak**	Units for Drift.
EDD_ID	
Format: Limited_List	*Required*
Record: **Header**	Must have the value DOE_EM_EDD. It can be checked by readers to determine that following data are in a DEEMS compatible format. Since this field need

DATA ELEMENT	DESCRIPTION
	not be the first line in a Header record, readers need to be prepared to read all the Header record lines before making this check.
EDD_Implementation_ID Format: Limited_List Record: **Header**	*Required* A value specified in a DEEMS implementation document as the identifier of the implementation. This value should be checked by readers to determine that following data are in a processible format. For example, an implementation might specify what records and data elements are required in the EDD, including any implementation defined fields. Since this field need not be the first line in a Header record, readers need to be prepared to read all the fields in this record before checking this value.
EDD_Implementation_Version Format: Limited_List Record: **Header**	*Required* A value specified in each revision of a DEEMS implementation document. The value in an EDD indicates the version of the implementation that following data is compatible with. Reader programs may have to adapt their behavior based on this value. In particular, the list of implementation defined fields may change with version number. Implementors should assign version numbers so that later versions have later alphabetical version numbers.
EDD_Version Format: Limited_List Record: **Header**	*Required* Specified in each revision of this document. Specified by the writer of an EDD to indicate the version of the DEEMS that following data is compatible with. Reader programs may have to adapt their behavior based on this value. In particular, the list of DEEMS defined fields may change with version number.
Efficiency Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analysis**	Efficiency of the instrument as a percent. Usually used in radiochemistry to mean the counts detected as a percentage of the decays actually occurring.
Record: **Analyte**	Same as in an Analysis record except applied to a specific analyte.
Record: **Peak**	Same as in an Analysis record except applied to a specific analyte and peak.
Energy	
Format: Numeric	
Record: **Peak**	The energy of an emission.
Record: **Peak_Comparison**	Same as in a Peak record.
Energy_Units	
Format: Limited_List	
Record: **Peak**	Units for Energy.
Record: **Peak_Comparison**	Units for Energy.
Equipment_Batch	
Format: Identifier	
Record: **Sample_and_Method**	An identifier for a batch of samples collected using the same equipment in a defined period of time. Operationally, this batch associates a field equipment blank with a group of samples. This value is currently often not known to the lab. It might be merged with lab data by a validator.
Field_Sample_ID	
Format: Identifier	
Record: **Sample_and_Method**	Identifier assigned to a sample by the sampler, not the client. This value is currently often not known to the lab. It could be useful as link into the sampling records system.
Final_Amount	
Format: Numeric	
Record: **Analysis**	The amount of sample remaining after final preparation for analysis.

DATA ELEMENT	DESCRIPTION
Record: **Cleanup**	Amount of material coming out of cleanup.
Final_Amount_Units Format: Limited_List	
Record: **Analysis**	Units for Final_Amount.
Record: **Cleanup**	Units for Final_Amount.
Flow_Rate Format: Numeric	
Record: **Analysis**	Rate of flow of gas or liquid mobile phase for GC or HPLC.
Flow_Rate_Units Format: Limited_List	
Record: **Analysis**	Units for Flow_Rate.
Fraction Format: Limited_List	
Record: **Sample_and_Method**	The fraction of a sample, based on a physical or chemical separation, to which the method is applied.
Frequency Format: Numeric	
Record: **Peak**	The frequency of an emission or absorption.
Record: **Peak_Comparison**	Same as in a Peak record.
Frequency_Units Format: Limited_List	
Record: **Peak**	Units for Frequency.
Record: **Peak_Comparison**	Units for Frequency.
Generating_System_ID Format: Identifier	
Record: **Header**	A lab defined value that identifies the software system used to generate the EDD. This value may be built into commercial software. The reader may use this value to adapt to known quirks of the generating system.

DATA ELEMENT	DESCRIPTION
Generating_System_Version Format: Text Record: **Header**	A lab defined version number for the software system used to generate the EDD.
Gradient Format: Numeric Record: **Analysis**	Temperature gradient for GC and mobile phase gradient for HPLC.
Gradient_Units Format: Limited_List Record: **Analysis**	Units for Gradient.
Handled Format: Date Record: **Handling**	Date of handling of this sample.
Handling_Batch Format: Identifier Record: **Handling**	The lab's identifier for a batch of samples handled together. The definition of a handling batch depends on the method but might be linked to handling specific QC samples. Example: All samples associated with one TCLP apparatus blank would be in one Handling_Batch of Cleanup_Type TCLP. The method QC sample in the batch might have QC_Type TCLP_Blank.
Handling_Duration Format: Numeric Record: **Handling**	The duration of the handling. Example: TCLP leaching time.
Handling_Duration_Units Format: Limited_List Record: **Handling**	Units for Handling_Duration.
Handling_Factor Format: Numeric Record: **Handling**	A factor that reflects processing done early in sample handling.

DATA ELEMENT	DESCRIPTION
	For example, used in radiochemistry with a hot lab that does preliminary processing prior to more routine activities.
Handling_Factor_Units Format: Limited_List Record: **Handling**	Units for Handling_Factor.
Handling_ID Format: Identifier Record: **Handling**	The lab's identifier for this handling event for this sample.
Handling_Type Format: Limited_List Record: **Sample_and_Method**	*Conditionally Required* For a method QC sample with QC_Linkage 'Handling_Batch', a code that identifies the type of handling this QC pertains to. The field's value must match that specified as the Handling_Type for handlings of associated samples.
Record: **Handling**	Code that describes preliminary processing done to a sample prior to aliquotting. Examples: Ashed, Decanted, Distilled, Drained, Dried, Filtered, Leached.
Heated_Purge Format: Limited_List Record: **Analysis**	Whether volatiles analysis used a heated purge.
Initial_Amount Format: Numeric Record: **Cleanup**	Amount of material going into cleanup.
Initial_Amount_Units Format: Limited_List Record: **Cleanup**	Units for Initial_Amount.
Injection_Volume Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analysis**	The volume of sample injected into the instrument.
Injection_Volume_Units Format: Limited_List Record: **Analysis**	Units for Injection_Volume.
Instrument_ID Format: Identifier Record: **Analysis**	The lab's code for an instrument.
Instrument_Serial_Number Format: Text Record: **Analysis**	The serial number of the instrument used for analysis. Note, this is not a numeric field.
Interelement_Correction Format: Limited_List Record: Analysis	Whether ICP interelement correction factors were applied.
Lab_Address Format: Text Record: **Sample_and_Method**	*Repeats OK* Address of the lab doing this analysis. May repeat in one record as needed to report a multi-line address.
Lab_Analysis_ID Format: Identifier Record: **Analysis**	*Required* The lab's identifier for an analysis. This value should be unique at least for all analyses in one lab reporting batch in the context of one method. Example: Lab file ID as used with GCMS analyses, planchet as used in radiochemistry.
Record: **Result**	If there is any ambiguity about which analysis underlies this result, the Lab_Analysis_ID of this analysis. Example: In CLP Inorganics, to identify from which of several dilutions the reported result is chosen.

DATA ELEMENT	DESCRIPTION
Lab_Analyte_ID	
Format: Identifier	*For traceability*
Record: **Result**	The lab's code for the analyte. This code gives traceability into the lab's systems.
Record: **Analyte**	Same as in a Result record.
Record: **Peak_Comparison**	Lab_Analyte_ID for the analyte to compare to. If not specified, it is assumed to be the same as the analyte for the Peak record this Peak_Comparison record is in.
Record: **Analyte_Comparison**	Lab_Analyte_ID for the analyte to compare to.
Lab_Contact	
Format: Text	
Record: **Sample_and_Method**	The person at the lab to contact with questions about this data.
Lab_Contract	
Format: Text	
Record: **Sample_and_Method**	Contract number under which the lab analyzes the samples. Client defined.
Lab_Data_Package_ID	
Format: Identifier	
Record: **Sample_and_Method**	Lab's code for the data package this data is part of. This code applies to a single deliverable. Use Lab_Reporting_Batch for the logical notion of a group of samples reported as a unit. For example, a document number the lab assigns to the physical data package or a file name for an electronic deliverable.
Lab_Data_Package_Name	
Format: Text	
Record: **Sample_and_Method**	Lab's title for the data package this data is part of.
Lab_Data_Package_Version	
Format: Text	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	If the lab resubmits a data package, this field can be used to distinguish the different versions.
Lab_ID	
Format: Limited_List	*Required*
Record: **Sample_and_Method**	Identifier for the lab doing this analysis. Often client defined.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Lab_Manager	
Format: Text	
Record: **Sample_and_Method**	The person at the lab who takes final responsibility for this data.
Lab_Manager_Title	
Format: Text	
Record: **Sample_and_Method**	The corporate title of the Lab_Manager.
Lab_Method_ID	
Format: Identifier	*For Traceability*
Record: **Sample_and_Method**	The lab's code for the method used. Unlike the Client_Method_ID, this ID is only used to identify work done in the context of a lab defined sample, so it need not have a globally defined meaning by itself.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Lab_Method_Name	
Format: Text	
Record: **Sample_and_Method**	The lab's descriptive name for this method.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Lab_Name	
Format: Text	
Record: **Sample_and_Method**	Descriptive name for the lab doing this analysis. Often lab defined.
Record: **Instrument_QC**	Same as in Sample_and_Method records.
Lab_Narrative_ID	
Format: Identifier	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Lab's code for any narrative document associated with this data.
Lab_Qualifier	
Format: Limited_List	*Repeats OK*
Record: **Result**	A result qualifier code assigned by the lab, based on client defined rules and values. This field may repeat as many times as needed to report multiple codes per result.
Record: **Analyte**	Same as in the Result record.
Record: **Peak**	Same as in the Result record.
Record: **Analyte_Comparison**	Same as in the Result record.
Record: **Peak_Comparison**	Same as in the Result record.
Lab_Qualifiers	
Format: Limited_List	
Record: **Result**	A string of single letter result qualifiers assigned by the lab, based on client defined rules and values.
Record: **Analyte**	Same as in the Result record.
Record: **Peak**	Same as in the Result record.
Record: **Analyte_Comparison**	Same as in the Result record.
Record: **Peak_Comparison**	Same as in the Result record.
Lab_Reanalysis_Suffix	
Format: Identifier	*For Traceability*
Record: **Sample_and_Method**	If the client wants results for reanalyses done by this method to be reported separately, the lab defined code to help identify the reanalysis. The Lab_Method_ID, Lab_Sample_ID and Lab_Reanalysis_Suffix together should uniquely identify the data associated with this record.
Lab_Receipt	
Format: Date	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Date the sample was received in the lab.
Lab Reported Format: Date Record: **Sample_and_Method**	Date these data were reported by the lab.
Lab_Reporting_Batch Format: Identifier Record: **Sample_and_Method**	An identifier for a batch of samples reported as a group by the lab. In addition to its use for administrative purposes, this batch can be used to link certain QC samples to regular ones, for example, a CLP storage blank. Example: Sample Delivery Group (SDG) as in the CLP.
Lab_Result_Status Format: Limited_List Record: **Sample_and_Method**	Lab assigned status, such as preliminary or final, for results for this sample and method. A client might define allowed values for this field.
Record: **Result**	Lab assigned status, such as preliminary or final, for this result. A client might define allowed values for this field.
Lab_Sample_ID Format: Identifier Record: **Sample_and_Method**	*For Traceability* Lab's identifier for a sample. This code is the primary link into the lab's record keeping system. It is not necessarily one-to-one with the Client_Sample_ID.
Level Format: Limited_List Record: **Sample_and_Method**	Approximate level of analytes in the sample, usually specified in client defined concentration ranges and determined via a screening procedure. Examples: Low, Medium, High.
Location_ID Format: Identifier	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Identifier for the sampling location at a site. Often client defined. Examples: Operable unit, well, tank, station, facility (building), installation, aggregate area.
Location_Name Format: Text Record: **Sample_and_Method**	Descriptive name for the sampling location at a site. May be lab defined. Examples: Operable unit, well, tank, station, facility (building), installation, aggregate area.
Lot_Number Format: Text Record: **Cleanup**	Manufacturer's batch number for something used in this cleanup. Example: Florisil cartridge lot number.
Mass_Charge_Ratio Format: Numeric Record: **Peak**	The mass/charge relationship recorded in MS detection.
Record: **Peak_Comparison**	Same as in a Peak record.
Matrix_ID Format: Limited_List Record: **Sample_and_Method**	*Required* A code for the sample matrix or media (e.g., soil, water). Should be client defined. This value, combined with the Client_Method_ID, defines to the reader method details that are implementation specific.
Matrix_Name Format: Text Record: **Sample_and_Method**	A description of the sample matrix or media. Often lab defined.
Melting_Point Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	The temperature at which the sample melts.
Melting_Point_Units Format: Limited_List Record: **Sample_and_Method**	Units for Melting_Point.
Method_Batch Format: Identifier Record: **Sample_and_Method**	An identifier for a batch of samples analyzed by one method and treated as a group for QC purposes. A method batch should group samples with similar matrices and potential interferences. This is a broader grouping than a preparation batch. In particular, a reanalysis of a sample stays in the same method batch, while it is likely to be in a different preparation batch. Operationally, this batch associates sample dependent QC such as duplicates and matrix spikes with a group of samples. Example: All samples of one matrix and level, analyzed by a CLP semivolatiles method and reported in one SDG.
Organism_Class Format: Limited_List Record: **Sample_and_Method**	A broad classification of a sample organism. Not necessarily intended to be the taxonomic class, but that is a possible value. Example: Animal, Commercial Animal, Fish, or Plant.
Organism_Length Format: Numeric Record: **Sample_and_Method**	Length of an organism.
Organism_Length_Units Format: Limited_List Record: **Sample_and_Method**	Units for Organism_Length.

DATA ELEMENT	DESCRIPTION
Organism_Portion Format: Limited_List Record: **Sample_and_Method**	Portion of an organism used for analysis.
Organism_Sex Format: Limited_List Record: **Sample_and_Method**	Sex of an organism: Male or Female.
Original_Client_Reanalysis_Type Format: Limited_List Record: **Sample_and_Method**	*Conditionally Required* For a method QC sample with QC_Category Duplicate, Serial_Dilution, Spike or Spike_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of Original_Client_Reanalysis_Type matches that of the Client_Reanalysis_Type for this original sample.
Original_Client_Sample_ID Format: Identifier Record: **Sample_and_Method**	*Conditionally Required* For a method QC sample of QC_Category Duplicate, Serial_Dilution, Spike or Spike_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of Original_Client_Sample_ID matches that of the Client_Sample_ID for this original sample. For a method QC sample of QC_Category Blank_Spike_Duplicate, the value of Original_Client_Sample_ID matches that of the Client_Sample_ID for the associated Blank_Spike.
Original_Lab_Reanalysis_Suffix Format: Identifier Record: **Sample_and_Method**	*For Traceability* For a method QC sample with QC_Category Duplicate, Serial_Dilution, Spike or Spike_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of Original_Lab_Reanalysis_Suffix matches that of the Lab_Reanalysis_Suffix for this original sample.
Original_Lab_Sample_ID	

DATA ELEMENT	DESCRIPTION
Format: Identifier Record: **Sample_and_Method**	For a method QC sample with QC_Category Duplicate, Serial_Dilution, Spike or Spike_Duplicate there must be an associated regular sample the QC sample is derived from. This sample is called the original. The value of Original_Lab_Sample_ID matches that of the Lab_Sample_ID for this original sample. For a method QC sample with QC_Category Blank_Spike_Duplicate, the value of Original_Lab_Sample_ID matches that of the Lab_Sample_ID for the associated Blank_Spike.
Peak_ID	
Format: Identifier Record: **Result**	*Conditionally Required* If there is any ambiguity about which peak underlies this result, the Peak_ID of that peak.
Record: **Analyte**	If there is any ambiguity about which peak underlies this analyte's result, the Peak_ID of that peak.
Record: **Peak**	A lab specified value, possibly based on client specified rules, that identifies a peak associated with an analyte. Peak_ID is conceptually similar to Client_Analyte_ID, except it identifies a peak rather than an analyte. Its value should be unique among all peaks for one analyte, but not necessarily have physical meaning. Examples: nominal mass for GCMS peaks, integer wavelength for ICP peaks, sequence number (1,2,...) for multicomponent GC peaks.
Record: **Peak_Comparison**	Peak identifier for the peak to compare to. It is combined with the Lab_Analyte_ID in the same Peak_Comparison record to fully specify the peak to compare to.
Percent_Breakdown	
Format: Numeric Record: **Analyte**	The percent breakdown (DDT/Endrin) reported for CLP pesticides.

DATA ELEMENT	DESCRIPTION
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Percent_Difference	
Format: Numeric	
Record: **Result**	The difference between two measured values as percentage of one of them. The denominator value is usually the more certain one, although details can be method specific. Used with method QC of QC_Category Serial Dilution.
Record: **Analyte**	Same as in Result records except applied to the results of analyses in an analysis group rather than a QC sample and original pair.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Record: **Peak_Comparison**	Same as in a Result record except used to compare values in two Peak_Comparison records.
Percent_Match	
Format: Numeric	
Record: **Analyte**	Percent match of an analyte as compared with a library mass spectrum.
Percent_Moisture	
Format: Numeric	
Record: **Sample_and_Method**	Percent of sample composed of water.
Record: **Handling**	Percent of sample composed of water after the handling described by this record.
Percent_Phase	
Format: Numeric	
Record: **Sample_and_Method**	Percent of sample in analyzed phase. This field may generalize ones like Percent_Solids.
Record: **Handling**	Percent of sample in analyzed phase after the handling described by this record.

DATA ELEMENT	DESCRIPTION
Percent_Preparation_Error	
Format: Numeric	
Record: **Analysis**	Same as in a Result record, except applies to all results from this analysis.
Record: **Result**	The uncertainty introduced into the final result by all lab activities other than instrumental analysis. Expressed as a percentage of the result value at one sigma.
Record: **Analyte**	Same as in a Result record.
Percent_Ratio	
Format: Numeric	
Record: **Peak_Comparison**	The response of the peak this Peak_Comparison record is in as a percentage of the response of the peak identified by the Peak_ID and Lab_Analyte_ID in this record. Used with mass spectral peaks in System Monitoring Compounds.
Percent_Recovery	
Format: Numeric	
Record: **Result**	For method QC of QC_Category Blank_Spike and Blank_Spike_Duplicate, the result as a percentage of the amount added. For method QC of QC_Category Spike and Spike_Duplicate, the spiked result minus the original result as a percentage of the amount added.
Record: **Analyte**	Same as in Result records except applied to the results from an analysis or analyses in an analysis group rather than a QC sample and original pair.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Percent_Relative_Abundance	
Format: Numeric	
Record: **Peak**	The response of this peak as a percentage of the largest peak response for this analyte.

DATA ELEMENT	DESCRIPTION
Percent_Relative_Standard_Deviation	
Format: Numeric	
Record: **Analyte**	The standard deviation as a percentage of the mean. Used for an analyte in an Analysis_Group record.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Record: **Peak_Comparison**	Same as in an Analyte record except applied to Peak_Comparison values.
Percent_Solids	
Format: Numeric	
Record: **Sample_and_Method**	Percent of the sample composed of solid material.
Record: **Handling**	Percent of the sample composed of solid material after the handling described by this record.
Percent_Valley	
Format: Numeric	
Record: **Analyte**	The valley between this analyte and another one, as a percentage of the height of the shorter one. The second analyte is assumed to be known based on the method.
Record: **Peak_Comparison**	The valley between the peak this Peak_Comparison record is in and the peak identified by the Peak_ID and Lab_Analyte_ID in this record as a percentage of the height of the shorter one.
pH	
Format: Numeric	
Record: **Sample_and_Method**	The negative of the logarithm of the hydrogen ion potential.
Record: **Handling**	Same as in a Sample_and_Method record.
Phase_Analyzed	
Format: Limited_List	
Record: **Sample_and_Method**	That portion of a multiphase sample actually analyzed.

DATA ELEMENT	DESCRIPTION
Preparation_Batch Format: Identifier Record: **Analysis**	An identifier for a batch of aliquots that are prepared together. For methods with no processing prior to analysis, the preparation batch can be simply a group of aliquots selected for analysis at roughly the same time. Preparation batches are used to link analyses of regular samples with lab generated method QC samples of QC_Category Blank, Blank_Spike and Blank_Spike_Duplicate, such as method blanks, lab control samples and duplicate lab control samples.
Preparation_Type Format: Limited_List Record: **Analysis**	A client defined code for the basic type of preparation done. Example: Extraction technique for semivolatiles. Could be a 3000 series SW-846 method code.
Prepared Format: Date Record: **Analysis**	Preparation date. Preparation is used generally to include method specific techniques such as extraction, digestion and separation.
Preservative Format: Text Record: **Sample_and_Method**	Preservative added to the sample.
Preserved_By Format: Text Record: **Sample_and_Method**	Organization that added preservative to the sample.
Priority_ID Format: Limited_List Record: **Sample_and_Method**	Client's code that identifies the priority assigned to this data. The priority may affect the desired turn around time and the cost of analysis.

DATA ELEMENT	DESCRIPTION
	Examples: Rush or quick turn around work.
Procedure_ID Format: Identifier	
Record: **Analysis**	Identifier for the lab's procedure (SOP) for this analysis.
Record: **Handling**	Identifier for the lab's procedure (SOP) for this handling.
Record: **Cleanup**	Identifier for the lab's procedure (SOP) for this cleanup.
Procedure_Name Format: Text	
Record: **Analysis**	Description of the lab's procedure (SOP) for this analysis.
Record: **Handling**	Description of the lab's procedure (SOP) for this handling.
Record: **Cleanup**	Description of the lab's procedure (SOP) for this cleanup.
Project_ID Format: Identifier	
Record: **Sample_and_Method**	Identifier for the project this sample is a part of. Often client defined. Typically, a project consists of samples from one site collected over some defined period of time. Examples: Case no, Episode, Sampling round.
Project_Name Format: Text	
Record: **Sample_and_Method**	Descriptive name for the project this sample is a part of. May be lab defined. Examples: Case no, Episode, Sampling round.

DATA ELEMENT	DESCRIPTION
QC_Category Format: Limited_List Record: **Sample_and_Method**	*For Portability* DEEMS defined code that specifies basic properties of a method QC sample. In a Sample_and_Method record, allowed values, with case ignored, are: Blank -- A QC sample with 'nothing' in it. Examples: Field, equipment, method (reagent), sulfur, and storage blanks. Blank_Spike -- A QC sample with a known amount added to a blank. Examples: lab control sample, QC check samples and interference check samples. Duplicate -- A reanalysis of a regular sample done for QC purposes. Examples: duplicates and splits. Blank_Spike Duplicate -- A reanalysis of a Blank_Spike. Serial_Dilution -- A dilution and reanalysis of a regular sample done for QC purposes. Spike -- A reanalysis of a regular sample with a known amount added and done for QC purposes. Examples: matrix spikes, post digestion spikes and analytical spikes. Spike_Duplicate -- A second reanalysis of a regular sample with a known amount added and done for QC purposes. There must be another sample with QC_Category "Spike" with the same original sample.
QC_Linkage Format: Limited_List Record: **Sample_and_Method**	*For Portability of QC* For a method QC sample, specifies which batch is the basis for the association between the QC sample and regular ones. Allowed values, ignoring case, include the following fields that define batches:

DATA ELEMENT	DESCRIPTION
	Sampling_Batch Equipment_Batch Shipping_Batch Lab_Reporting_Batch Method_Batch Handling_Batch Preparation_Batch Analysis_Batch If QC_Linkage is 'Handling_Batch', there should be a Handling_Type field in the Sample_and_Method record whose value clarifies which type of handling batch is intended. Example: In a Sample_and_Method record, if the QC_Type is Lab_Duplicate, the QC_Category is Duplicate and the QC_Linkage is Method_Batch, a reader knows that this data for is a client defined type of QC called a Lab_Duplicate, that it is processed with rules typical for Duplicates and that it is to be associated with other Sample_and_Method records with the same value for the Method_Batch field. QC_Linkage is most useful if the batch it names is a required field in appropriate records, based on implementation rules. The correct linkage for a field QC sample may not be known to the lab, so must be merged with lab data at a later time.
Record: **Instrument_QC**	Same as in a Sample_and_Method Record except allowed values for instrument QC, ignoring case, are Cleanup_Batch, Preparation_Batch, Analysis_Batch and Run_Batch. If QC_Linkage is 'Cleanup_Batch', there should be a Cleanup_Type field in the Instrument_QC record whose value clarifies which type of cleanup batch is intended.
QC_Type	

DATA ELEMENT	DESCRIPTION
Format: Limited_List	
Record: **Sample_and_Method**	For a method QC sample, the client's code for the type of QC. In the context of the Client_Method_ID and Matrix_ID, this code determines all special processing rules for the QC sample. The presence of this field in the Sample_and_Method record with a value allowed by the implementation defines the sample as a method QC sample. A lab may not know that certain samples are field QC. In this case the lab reports them as regular samples and their type is changed later, possibly by the validator.
Record: **Instrument_QC**	For instrument QC, a client defined code that specifies what type of instrument QC data follows. In the context of the Client_Method_ID, the value must imply enough detail for the reader to understand the method specific details of the following Analysis_Group, Analysis, Cleanup, Analyte, Peak, Peak_Comparison and Analyte_Comparison records.
Quantitation_Limit	
Format: Numeric	
Record: **Result**	Quantitation limit for the analyte being measured.
Record: **Analyte**	Same as in a Result record extended to anything considered to be the result of any analysis. Within an Analysis_Group record, applies to a mean or other value computed from several analyses.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Quantitation_Limit_Type	
Format: Limited_List	
Record: **Result**	One of a list of client defined acronyms that specify the type of quantitation limit. Examples: CRQL, PQL, SQL.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.

DATA ELEMENT	DESCRIPTION
Quantitation_Limit_Units	
Format: Limited_List	
Record: **Result**	Units for Quantitation_Limit. If the client specifies that the Quantitation_Limit_Units must be the same as the Result_Units, the Quantitation_Limit_Units need not be specified.
Record: **Analyte**	Same as in a Result record
Record: **Peak**	Same as in a Result record.
Quench	
Format: Numeric	
Record: **Analysis**	Result of quench calculation for scintillation counters.
Refractive_Index	
Format: Numeric	
Record: **Sample_and_Method**	Refractive index of sample.
Relative_Percent_Difference	
Format: Numeric	
Record: **Result**	The absolute value of the difference of two values as a percentage of their average. Used with method QC of QC_Category Duplicate, Spike_Duplicate and Blank_Spike_Duplicate.
Record: **Analyte**	Same as in Result records except applied to the results of analyses in an analysis group rather than a QC sample and original pair.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Record: **Peak_Comparison**	Same as in a Result record except used to compare values in two Peak_Comparison records.
Relative_Response_Factor	
Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analyte**	The relative response factor for this analyte, based on the assumption that the method specifies the analyte to compare to and which peaks to use.
Record: **Peak_Comparison**	The relative response factor of the peak this Peak_Comparison record is in compared to the peak identified by the Peak_ID and Lab_Analyte_ID in this record. A relative response factor is the ratio of two response factors, one for each peak. A response factor is the ratio of a response to an amount added.
Requestor_ID Format: Identifier Record: **Sample_and_Method**	An identifier for the organization that requested that this sample be analyzed. May not be the same as the client, which specifies the SOW to follow.
Requestor_Name Format: Text Record: **Sample_and_Method**	A name for the organization that requested that this sample be analyzed.
Required_Detection_Limit Format: Numeric Record: **Result**	A contractually specified upper limit for the detection limit for the analyte being measured. Depending on client and method specific rules, required detection limits might be scaled by factors such as dilution and percent moisture prior to reporting.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Required_Detection_Limit_Units Format: Limited_List Record: **Result**	Units for Required_Detection_Limit. If the client specifies that the Required_Detection_Limit_Units must be the same as

DATA ELEMENT	DESCRIPTION
	the Result_Units, the Detection_Limit_Units need not be specified.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Residue	
Format: Numeric	
Record: **Analysis**	Solid material remaining after preparation of an aliquot.
Residue_Units	
Format: Limited_List	
Record: **Analysis**	Units for Residue.
Resolution	
Format: Numeric	
Record: **Analysis**	A possibly sample and method dependent estimate of the resolution of the instrument used in the analysis. For example, in isotopic alpha spectroscopy, the width of the tracer peak.
Record: **Analyte**	A possibly sample and method dependent estimate of the resolution of the instrument that applies to the analysis and analyte.
Record: **Peak**	Resolution for this peak. Details of how resolution is computed depend on the method.
Resolution_Units	
Format: Limited_List	
Record: **Analysis**	Units for Resolution.
Record: **Analyte**	Units for Resolution.
Record: **Peak**	Units for Resolution.
Response	
Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analyte**	Response from a detector. Can be any type of response from ICP, AA, GC, MS, etc. Often, these are unitless numbers relating to a signal from the detector. Examples: Area, height, count rate.
Record: **Peak**	Same as in an Analyte record, except for a single peak. Example: individual Aroclor peak concentrations used for CLP reporting.
Response_Units	
Format: Limited_List	
Record: **Analyte**	Units for Response.
Record: **Peak**	Units for Response.
Result	
Format: Numeric	
Record: **Result**	Reportable result for the analyte. Example: Concentration.
Record: **Analyte**	Same as in a Result record extended to anything considered to be the result of any analysis. Within an Analysis_Group record, applies to a mean or other value computed from several analyses.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Result_Limit_Lower	
Format: Numeric	
Record: **Result**	Lower limit for a result based on external knowledge about the sample. Units are the same as for Results.
Record: **Analyte**	Same as in the Result record.
Result_Limit_Upper	
Format: Numeric	
Record: **Result**	Upper limit for a result based on external knowledge about the sample. Units are the same as for Results.

DATA ELEMENT	DESCRIPTION
Record: **Analyte**	Same as in the Result record.
Result_Units Format: Limited_List Record: **Result**	Units for Result.
Record: **Analyte**	Same as in a Result record.
Record: **Peak**	Same as in a Result record.
Retention_Time Format: Numeric Record: **Result**	The time between injection and detection for mobile phase separation techniques such as GC and HPLC. (Time format hh:mm:ss is not allowed.) In a result record, this is the retention time from the analysis underlying this result.
Record: **Analyte**	Same as in a result record. Used when there is a well defined retention time for the analyte, not just for a peak measurement for the analyte. For example, this applies to GCMS analyses.
Record: **Peak**	Same as in a Result record except for a single peak. Used with techniques like GC where there can be multiple peaks with different retention times for one analyte.
Retention_Time_High Format: Numeric Record: **Analyte**	High limit for a retention time window. Units are specified with Retention_Time_Units.
Record: **Peak**	Same as in an Analyte record, except for a single peak.
Retention_Time_Low Format: Numeric Record: **Analyte**	Low limit for a retention time window. Units are specified with Retention_Time_Units.
Record: **Peak**	Same as in an Analyte record, except for a single peak.

DATA ELEMENT	DESCRIPTION
Retention_Time_Units	
Format: Limited_List	
Record: **Result**	Units for Retention_Time.
Record: **Analyte**	Units for Retention_Time.
Record: **Peak**	Units for Retention_Time.
Run_Batch	
Format: Identifier	
Record: **Analysis**	An identifier for a batch of analyses that make up a run, a sequence of analyses during which the instrument is continuously in control. Example: A batch of samples analyzed on one instrument under the control of one initial calibration or similar Instrument_QC.
Sample_Amount	
Format: Numeric	
Record: **Sample_and_Method**	Weight or volume of sample as received by the lab.
Record: **Handling**	Weight or volume of sample after the handling described by this record.
Sample_Amount_Units	
Format: Limited_List	
Record: **Sample_and_Method**	Units for Sample_Amount.
Record: **Handling**	Units for the Sample_Amount.
Sampling_Batch	
Format: Identifier	
Record: **Sample_and_Method**	An identifier for a batch of samples collected together. Operationally, this batch associates a field blank with a group of samples. This value is currently often not known to the lab. It might be merged with lab data by a validator.
Screen_Value	
Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Result from a screening analysis of the sample, as in an alpha particle screen.
Screen_Value_Units Format: Limited_List Record: **Sample_and_Method**	Units for Screen_Value.
Services_ID Format: Identifier Record: **Sample_and_Method**	Client's code for optional services performed for this data. This includes nonstandard work, such as modified detection limits, or changed QC requirements. Examples: Special Analytical Services (SAS) number or Analytical Service Level.
Shipping_Batch Format: Identifier Record: **Sample_and_Method**	An identifier for a batch of samples shipped together, such as in the same crate, cooler or ice chest. Operationally, this batch associates a trip blank with a group of samples. This value, as defined by the shippers, is currently often not known to the lab. It might be merged with lab data by a validator.
Site_ID Format: Identifier Record: **Sample_and_Method**	Identifier for the broadly defined site where the sample was collected. Often client defined.
Site_Name Format: Text Record: **Sample_and_Method**	Descriptive name for the broadly defined site where the sample was collected. May be lab defined.
Standard_Deviation Format: Numeric	

DATA ELEMENT	DESCRIPTION
Record: **Analyte**	The standard deviation of several measurements of one analyte. Used for an analyte in an Analysis_Group record.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Record: **Peak_Comparison**	Same as in an Analyte record when reporting peak comparisons.

Standard_Deviation_Units
Format: Limited_List

Record: **Analyte**	Units for Standard_Deviation. If the client specifies that the Standard_Deviation_Units must be the same as the Result_Units, the Standard_Deviation_Units need not be specified.
Record: **Peak**	Same as in an Analyte record when results are measured per peak.
Record: **Peak_Comparison**	Same as in an Analyte record except applied to Peak_Comparison values.

Standard_ID
Format: Identifier

Record: **Analysis**	Lab's identification for a standard, such as a spiking material, used in this analysis.

Standard_Source
Format: Text

Record: **Analysis**	Source for a standard used in this analysis.

Suspended_Solids
Format: Numeric

Record: **Sample_and_Method**	Solids remaining on the filter paper after filtration of a water or other liquid sample.
Record: **Handling**	Same as in a Sample_and_Method record.

Suspended_Solids_Units
Format: Limited_List

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Units for Suspended_Solids.
Record: **Handling**	Units for Suspended_Solids.
Temperature Format: Numeric Record: **Sample_and_Method**	Temperature of the sample as received.
Temperature_units Format: Limited_List Record: **Sample_and_Method**	Units for temperature.
Texture Format: Limited_List Record: **Sample_and_Method**	Descriptive information about a solid sample. Example: Fine, medium and coarse; or: boulder, pebble and sand; or: round and angular; or uniform and irregular.
Record: **Handling**	Descriptive information about a solid sample after the handling described by this record.
Turbidity Format: Numeric Record: **Sample_and_Method**	Turbidity of the sample.
Turbidity_Units Format: Limited_List Record: **Sample_and_Method**	Units for Turbidity.
Validated Format: Date Record: **Sample_and_Method**	Date validation completed.
Validation_Qualifier Format: Limited_List Record: **Result**	*Repeats OK* A result qualifier code assigned by the validator, based on client defined rules and values. This field is only used with results for regular samples. This field may

DATA ELEMENT	DESCRIPTION
	repeat as many times as needed per result to report multiple codes.
Validation_Qualifiers Format: Limited_List Record: **Result**	A string of single letter result qualifiers assigned by the validator, based on client defined rules and values. This field is only used with results for regular samples.
Validator_Address Format: Text Record: **Sample_and_Method**	*Repeats OK* Address of the validator doing the validation. May repeat in one record as needed to report a multi-line address.
Validator_Contact Format: Text Record: **Sample_and_Method**	The person at the validator to contact with questions about this data.
Validator_Contract Format: Text Record: **Sample_and_Method**	Contract number under which the validator validates the samples. Client defined.
Validator_Data_Package_ID Format: Identifier Record: **Sample_and _Method**	Validator's code for the data package this data is part of.
Validator_Data_Package_Name Format: Text Record: **Sample_and_Method**	Validator's title for the data package this data is part of.
Validator_Data_Package_Version Format: Text Record: **Sample_and_Method**	If the validator resubmits a data package, this field can be used to distinguish the different versions.
Validator_ID Format: Limited_List	

DATA ELEMENT	DESCRIPTION
Record: **Sample_and_Method**	Identification for the validator doing the validation. Often client defined. This and other 'validator_' fields are not typically known to the lab. They are included for use by validators who might receive a lab EDD, validate it and pass on an updated EDD to the client.
Validator_Manager Format: Text Record: **Sample_and_Method**	The person at the validator who takes final responsibility for this data.
Validator_Manager_Title Format: Text Record: **Sample_and_Method**	The corporate title of the Validator_Manager.
Validator_Method_ID Format: Identifier Record: Sample_and_Method	The validator's code for the work it does.
Validator_Method_Name Format: Text Record: **Sample_and_Method**	The validator's descriptive name for the work it does when validating data analyzed by this method.
Validator_Name Format: Text Record: **Sample_and_Method**	Descriptive name for the validator doing the validation. Often validator defined.
Validator_Narrative_ID Format: Identifier Record: **Sample_and_Method**	Validator's code for any narrative document associated with this data.
Validator_Receipt Format: Date Record: **Sample_and_Method**	Date sample data received by the validator.
Validator_Reported	

DATA ELEMENT	DESCRIPTION
Format: Date	
Record: **Sample_and_Method**	Date this work reported by the validator.
Wavelength	
Format: Numeric	
Record: **Peak**	The wavelength used for an analytical measurement; e.g., UV/vis, GFAA and ICP.
Record: **Peak_Comparison**	Same as in a Peak record.
Wavelength_Units	
Format: Limited_List	
Record: **Peak**	Units for Wavelength.
Record: **Peak_Comparison**	Units for Wavelength.
Yield	
Format: Numeric	
Record: **Analysis**	A measure of the success of the preparation part of the method as a percent. For radiochemistry, the number of atoms of interest making it through sample preparation as a percentage of the number in the aliquot.